

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: FROMMER, Wolf-Bernd
- (ii) TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO ACID
TRANSPORTER, PLASMIDS, BACTERIA, YEASTS AND PLANTS
CONTAINING A TRANSPORTER AND THEIR USE
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
 - (B) STREET: 1180 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: NY
 - (E) COUNTRY: US
 - (F) ZIP: 10036-8403
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/362,512
 - (B) FILING DATE: 05-JAN-1995
 - (C) CLASSIFICATION: 800
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/007,636
 - (B) FILING DATE: 21-JAN-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Meilman, Edward A.
 - (B) REGISTRATION NUMBER: 24,735
 - (C) REFERENCE/DOCKET NUMBER: P/951-107
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 382-0700
 - (B) TELEFAX: (212) 382-0888
 - (C) TELEX: 236925

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1685 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliano

05474-05474

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 57..1511

(D) OTHER INFORMATION: /note= "amino acid transporter"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTTAAAACAT TTATTTTATC TTCTTCTTGT TCTCTCTTTC TCTTTCTCTC ATCACT	56
ATG AAG AGT TTC AAC ACA GAA GGA CAC AAC CAC TCC ACG GCG GAA TCC Met Lys Ser Phe Asn Thr Glu Gly His Asn His Ser Thr Ala Glu Ser	104
1 5 10 15	
GGC GAT GCC TAC ACC GTG TCG GAC CCG ACA AAG AAC GTC GAT GAA GAT Gly Asp Ala Tyr Thr Val Ser Asp Pro Thr Lys Asn Val Asp Glu Asp	152
20 25 30	
GGT CGA GAG AAG CGT ACC GGG ACG TGG CTT ACG GCG AGT GCG CAT ATT Gly Arg Glu Lys Arg Thr Gly Thr Trp Leu Thr Ala Ser Ala His Ile	200
35 40 45	
ATC ACG GCG GTG ATA GGC TCC GGA GTG TTG TCT TTA GCA TGG GCT ATA Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile	248
50 55 60	
GCT CAG CTT GGT TGG ATC GCA GGG ACA TCG ATC TTA CTC ATT TTC TCG Ala Gln Leu Gly Trp Ile Ala Gly Thr Ser Ile Leu Leu Ile Phe Ser	296
65 70 75 80	
TTC ATT ACT TAC TTC ACC TCC ACC ATG CTT GCC GAT TGC TAC CGT GCG Phe Ile Thr Tyr Phe Thr Ser Thr Met Leu Ala Asp Cys Tyr Arg Ala	344
85 90 95	
CCG GAT CCC GTC ACC GGA AAA CGG AAT TAC ACT TAC ATG GAC GTT GTT Pro Asp Pro Val Thr Gly Lys Arg Asn Tyr Thr Tyr Met Asp Val Val	392
100 105 110	
CGA TCT TAC CTC GGT GGT AGG AAA GTG CAG CTC TGT GGA GTG GCA CAA Arg Ser Tyr Leu Gly Gly Arg Lys Val Gln Leu Cys Gly Val Ala Gln	440
115 120 125	
TAT GGG AAT CTG ATT GGG GTC ACT GTT GGT TAC ACC ATC ACT GCT TCT Tyr Gly Asn Leu Ile Gly Val Thr Val Gly Tyr Thr Ile Thr Ala Ser	488
130 135 140	
ATT AGT TTG GTA GCG GTA GGG AAA TCG AAC TGC TTC CAC GAT AAA GGG Ile Ser Leu Val Ala Val Gly Lys Ser Asn Cys Phe His Asp Lys Gly	536
145 150 155 160	
CAC ACT GCG GAT TGT ACT ATA TCG AAT TAT CCG TAT ATG GCG GTT TTT His Thr Ala Asp Cys Thr Ile Ser Asn Tyr Pro Tyr Met Ala Val Phe	584
165 170 175	
GGT ATC ATT CAA GTT ATT CTT AGC CAG ATC CCA AAT TTC CAC AAG CTC Gly Ile Ile Gln Val Ile Leu Ser Gln Ile Pro Asn Phe His Lys Leu	632
180 185 190	
TCT TTT CTT TCC ATT ATG GCC GCA GTC ATG TCC TTT ACT TAT GCA ACT Ser Phe Leu Ser Ile Met Ala Ala Val Met Ser Phe Thr Tyr Ala Thr	680

4445350

195	200	205	
ATT GGA ATC GGT CTA GCC ATC GCA ACC GTC GCA GGT GGG AAA GTG GGT Ile Gly Ile Gly Leu Ala Ile Ala Thr Val Ala Gly Gly Lys Val Gly 210 215 220			728
AAG ACG AGT ATG ACG GGC ACA GCG GTT GGA GTA GAT GTA ACC GCA GCT Lys Thr Ser Met Thr Gly Thr Ala Val Gly Val Asp Val Thr Ala Ala 225 230 235 240			776
CAA AAG ATA TGG AGA TCG TTT CAA GCG GTT GGG GAC ATA GCG TTC GCC Gln Lys Ile Trp Arg Ser Phe Gln Ala Val Gly Asp Ile Ala Phe Ala 245 250 255			824
TAT GCT TAT GCC ACG GTT CTC ATC GAG ATT CAG GAT ACA CTA AGA TCT Tyr Ala Tyr Ala Thr Val Leu Ile Glu Ile Gln Asp Thr Leu Arg Ser 260 265 270			872
AGC CCA GCT GAG AAC AAA GCC ATG AAA AGA GCA AGT CTT GTG GGA GTA Ser Pro Ala Glu Asn Lys Ala Met Lys Arg Ala Ser Leu Val Gly Val 275 280 285			920
TCA ACC ACC ACT TTT TTC TAC ATC TTA TGT GGA TGC ATC GGC TAT GCT Ser Thr Thr Thr Phe Phe Tyr Ile Leu Cys Gly Cys Ile Gly Tyr Ala 290 295 300			968
GCA TTT GGA AAC AAT GCC CCT GGA GAT TTC CTC ACA GAT TTC GGG TTT Ala Phe Gly Asn Asn Ala Pro Gly Asp Phe Leu Thr Asp Phe Gly Phe 305 310 315 320			1016
TTC GAG CCC TTT TGG CTC ATT GAC TTT GCA AAC GCT TGC ATC GCT GTC Phe Glu Pro Phe Trp Leu Ile Asp Phe Ala Asn Ala Cys Ile Ala Val 325 330 335			1064
CAC CTT ATT GGT GCC TAT CAG GTG TTC GCG CAG CCG ATA TTC CAG TTT His Leu Ile Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Gln Phe 340 345 350			1112
GAT GAG AAA AAA TGC AAC AGA AAC TAT CCA GAC AAC AAG TTC ATC ACT Val Glu Lys Lys Cys Asn Arg Asn Tyr Pro Asp Asn Lys Phe Ile Thr 355 360 365			1160
TCT GAA TAT TCA GTA AAC GTA CCT TTC CTT GGA AAA TTC AAC ATT AGC Ser Glu Tyr Ser Val Asn Val Pro Phe Leu Gly Lys Phe Asn Ile Ser 370 375 380			1208
CTC TTC AGA TTG GTG TGG AGG ACA GCT TAT GTG GTT ATA ACC ACT GTT Leu Phe Arg Leu Val Trp Arg Thr Ala Tyr Val Val Ile Thr Thr Val 385 390 395 400			1256
GTA GCT ATG ATA TTC CCT TTC TTC AAC GCG ATC TTA GGT CTT ATC GGA Val Ala Met Ile Phe Pro Phe Phe Asn Ala Ile Leu Gly Leu Ile Gly 405 410 415			1304
GCA GCT TCC TTC TGG CCT TTA ACG GTT TAT TTC CCT GTG GAG ATG CAC Ala Ala Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met His 420 425 430			1352
ATT GCA CAA ACC AAG ATT AAG AAG TAC TCT GCT AGA TGG ATT GCG CTG Ile Ala Gln Thr Lys Ile Lys Lys Tyr Ser Ala Arg Trp Ile Ala Leu			1400

145	150								155					160			
His	Thr	Ala	Asp	Cys 165	Thr	Ile	Ser	Asn 170	Tyr	Pro	Tyr	Met	Ala	Val 175	Phe		
Gly	Ile	Ile	Gln 180	Val	Ile	Leu	Ser	Gln 185	Ile	Pro	Asn	Phe	His 190	Lys	Leu		
Ser	Phe	Leu	Ser	Ile	Met	Ala	Ala 200	Val	Met	Ser	Phe	Thr 205	Tyr	Ala	Thr		
Ile	Gly 210	Ile	Gly	Leu	Ala	Ile 215	Ala	Thr	Val	Ala	Gly 220	Gly	Lys	Val	Gly		
Lys 225	Thr	Ser	Met	Thr	Gly 230	Thr	Ala	Val	Gly	Val 235	Asp	Val	Thr	Ala	Ala 240		
Gln	Lys	Ile	Trp	Arg 245	Ser	Phe	Gln	Ala	Val 250	Gly	Asp	Ile	Ala	Phe 255	Ala		
r	Ala	Tyr	Ala 260	Thr	Val	Leu	Ile	Glu 265	Ile	Gln	Asp	Thr	Leu 270	Arg	Ser		
Ser	Pro	Ala 275	Glu	Asn	Lys	Ala	Met 280	Lys	Arg	Ala	Ser	Leu 285	Val	Gly	Val		
Ser	Thr 290	Thr	Thr	Phe	Phe	Tyr 295	Ile	Leu	Cys	Gly	Cys 300	Ile	Gly	Tyr	Ala		
Ala 305	Phe	Gly	Asn	Asn	Ala 310	Pro	Gly	Asp	Phe	Leu 315	Thr	Asp	Phe	Gly	Phe 320		
Phe	Glu	Pro	Phe	Trp 325	Leu	Ile	Asp	Phe	Ala 330	Asn	Ala	Cys	Ile	Ala 335	Val		
His	Leu	Ile	Gly 340	Ala	Tyr	Gln	Val	Phe 345	Ala	Gln	Pro	Ile	Phe 350	Gln	Phe		
Val	Glu	Lys 355	Lys	Cys	Asn	Arg	Asn 360	Tyr	Pro	Asp	Asn	Lys 365	Phe	Ile	Thr		
Ser	Glu 370	Tyr	Ser	Val	Asn	Val 375	Pro	Phe	Leu	Gly	Lys 380	Phe	Asn	Ile	Ser		
Leu 385	Phe	Arg	Leu	Val	Trp 390	Arg	Thr	Ala	Tyr	Val 395	Val	Ile	Thr	Thr	Val 400		
Val	Ala	Met	Ile	Phe 405	Pro	Phe	Phe	Asn 410	Ala	Ile	Leu	Gly	Leu	Ile 415	Gly		
Ala	Ala	Ser	Phe 420	Trp	Pro	Leu	Thr	Val 425	Tyr	Phe	Pro	Val	Glu 430	Met	His		
Ile	Ala	Gln 435	Thr	Lys	Ile	Lys	Lys 440	Tyr	Ser	Ala	Arg	Trp 445	Ile	Ala	Leu		
Lys	Thr 450	Met	Cys	Tyr	Val	Cys 455	Leu	Ile	Val	Ser	Leu 460	Leu	Ala	Ala	Ala		
Gly	Ser	Ile	Ala	Gly	Leu	Ile	Ser	Ser	Val	Lys	Thr	Tyr	Lys	Pro	Phe		

480

(2) INFORMATION FOR SEO ID NO:3:

(D) TOPOLOGY: linear

(A) ORGANISM: *Arabidopsis thaliana*

(D) OTHER INFORMATION: /product= "amino acid transporter"

GCA GTG TCT GGC AAG AGA AAC TAC ACT TAC ATG GAT GCC GTT CGA TCA 448
Ala Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ser
110 115 120

ATT Ile	CTC Leu	GGT Gly	GGG Gly	TTC Phe	AAG Lys	TCT Phe	AAG Lys	ATT Ile	TGT Cys	GGG Gly	TTG Leu	ATT Ile	TAA Gln	TAC Tyr	TTG Leu	496
AAT Asn	CTC Leu	TTT Phe	GGT Gly	ATC Ile	GCA Ala	ATT Ile	GGA Gly	TAC Tyr	ACG Thr	ATA Ile	GCA Ala	GCT Ala	TCC Ser	ATA Ile	AGC Ser	544
ATG Met	ATG Met	GCG Ala	ATC Ile	AAG Lys	AGA Arg	TCC Ser	AAC Asn	TGC Cys	TTC Phe	CAC His	AAG Lys	AGT Ser	GGA Gly	GGA Gly	AAA Lys	592
GAC Asp	CCA Pro	TGT Cys	CAC His	ATG Met	TCC Ser	AGT Ser	AAT Asn	CCT Pro	TAC Tyr	ATG Met	ATC Ile	GTA Val	TTT Phe	GGT Gly	GTG Val	640
GCA Ala	GAG Glu	ATC Ile	TTG Leu	CTC Leu	TCT Ser	CAG Gln	GTT Val	CCT Pro	GAT Asp	TTC Phe	GAT Asp	CAG Gln	ATT Ile	TGG Trp	TGG Trp	688
TCC Ser	ATT Ile	GTT Val	GCA Ala	GCT Ala	GTT Val	ATG Met	TCC Ser	TTC Phe	ACT Thr	TAC Tyr	TCT Ser	GCC Ala	ATT Ile	GGT Gly		736
CTA Leu	GCT Ala	CTT Leu	GGA Gly	ATC Ile	GTT Val	CAA Gln	GTT Val	GCA Ala	GCG Ala	AAT Asn	GGA Gly	GTT Val	TTC Phe	AAA Lys	GGA Gly	784
AGT Ser	CTC Leu	ACT Thr	GGA Gly	ATA Ile	AGC Ser	ATC Ile	GGA Gly	ACA Thr	GTG Val	ACT Thr	CAA Gln	ACA Thr	CAG Gln	AAG Lys	ATA Ile	832
TGG Trp	AGA Arg	ACC Thr	TTC Phe	CAA Gln	GCA Ala	CTT Leu	GGA Gly	GAC Asp	ATT Ile	GCC Ala	TTT Phe	GCG Ala	TAC Tyr	TCA Ser	TAC Tyr	880
TCT Ser	GTT Val	GTC Val	CTA Leu	ATC Ile	GAG Glu	ATT Ile	CAG Gln	GAT Asp	ACT Thr	GTA Val	AGA Arg	TCC Ser	CCA Pro	CCG Pro	GCG Ala	928
GAA Glu	TCG Ser	AAA Lys	ACG Thr	ATG Met	AAG Lys	AAA Lys	GCA Ala	ACA Thr	AAA Lys	ATC Ile	AGT Ser	ATT Ile	GCC Ala	GTC Val	ACA Thr	976
ACT Thr	ATC Ile	TTC Phe	TAC Tyr	ATG Met	CTA Leu	TGT Cys	GGC Gly	TCA Ser	ATG Met	GGT Gly	TAT Tyr	GCC Ala	GCT Ala	TTT Phe	GGA Gly	1024
GAT Asp	GCA Ala	GCA Ala	CCG Pro	GGA Gly	AAC Asn	CTC Leu	CTC Leu	ACC Thr	GGT Gly	TTT Phe	GGA Gly	TTC Phe	TAC Tyr	AAC Asn	CCG Pro	1072
TTT Phe	TGG Trp	CTC Leu	CTT Leu	GAC Asp	ATA Ile	GCT Ala	AAC Asn	GCC Ala	GCC Ala	ATT Ile	GTT Val	GTC Val	CAC His	CTC Leu	GTT Val	1120
GGA Gly	GCT Ala	TAC Tyr	CAA Gln	GTC Val	TTT Phe	GCT Ala	CAG Gln	CCC Pro	ATC Ile	TTT Phe	GCC Ala	TTT Phe	ATT Ile	GAA Glu	AAA Lys	1168

TCA GTC GCA GAG AGA TAT C A GAC AAT GAC TTC CTC AGC AG GAA TTT Ser Val Ala Glu Arg Tyr Pro Asp Asn Asp Phe Leu Ser Lys Glu Phe 365 370 375	1216
GAA ATC AGA ATC CCC GGA TTT AAG TCT CCT TAC AAA GTA AAC GTT TTC Glu Ile Arg Ile Pro Gly Phe Lys Ser Pro Tyr Lys Val Asn Val Phe 380 385 390 395	1264
AGG ATG GTT TAC AGG AGT GGC TTT GTC GTT ACA ACC ACC GTG ATA TCG Arg Met Val Tyr Arg Ser Gly Phe Val Val Thr Thr Thr Val Ile Ser 400 405 410	1312
ATG CTG ATG CCG TTT TTT AAC GAC GTG GTC GGG ATC TTA GGG GCG TTA Met Leu Met Pro Phe Phe Asn Asp Val Val Gly Ile Leu Gly Ala Leu 415 420 425	1360
GGG TTT TGG CCC TTG ACG GTT TAT TTT CCG GTG GAG ATG TAT ATT AAG Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Lys 430 435 440	1408
C C AGG AAG GTT GAG AAA TGG AGC ACG AGA TGG GTG TGT TTA CAG ATG C A Arg Lys Val Glu Lys Trp Ser Thr Arg Trp Val Cys Leu Gln Met 445 450 455	1456
CTT AGT GTT GCT TGT CTT GTG ATC TCG GTG GTC GCC GGG GTT GGA TCA Leu Ser Val Ala Cys Leu Val Ile Ser Val Val Ala Gly Val Gly Ser 460 465 470 475	1504
ATC GCC GGA GTG ATG CTT GAT CTT AAG GTC TAT AAG CCA TTC AAG TCT Ile Ala Gly Val Met Leu Asp Leu Lys Val Tyr Lys Pro Phe Lys Ser 480 485 490	1552
ACA TAT TGATGATTAT GGACCATGAA CAACAGAGAG AGTTGGTGTG TAAAGTTTAC Thr Tyr	1608
CATTTCAAAG AAAACTCCAA AAATGTGTAT ATTGTATGTT GTTCTCATTT CGTATGGTCT	1668
CATCTTTGTA ATAAAATTTA AAACCTATGT TATAAATTAT AAAAAAAAAA AAAAAAAAAA	1728
AAAAAAAAAA AA	1740

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gly	Glu	Thr	Ala	Ala	Ala	Asn	Asn	His	Arg	His	His	His	His	His
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Gly	His	Gln	Val	Phe	Asp	Val	Ala	Ser	His	Asp	Phe	Val	Pro	Pro	Gln
			20					25					30		

104150-0540

Pro Ala Phe Lys Cys Phe . . p Asp Asp Gly Arg Leu Lys .rg Thr Gly
 35 40 45
 Thr Val Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser
 50 55 60
 Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly Trp Ile Ala
 65 70 75 80
 Gly Pro Ala Val Met Leu Leu Phe Ser Leu Val Thr Leu Tyr Ser Ser
 85 90 95
 Thr Leu Leu Ser Asp Cys Tyr Arg Thr Gly Asp Ala Val Ser Gly Lys
 100 105 110
 Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ser Ile Leu Gly Gly Phe
 115 120 125
 Lys Phe Lys Ile Cys Gly Leu Ile Gln Tyr Leu Asn Leu Phe Gly Ile
 130 135 140
 . . Ile Gly Tyr Thr Ile Ala Ala Ser Ile Ser Met Met Ala Ile Lys
 145 150 155 160
 Arg Ser Asn Cys Phe His Lys Ser Gly Gly Lys Asp Pro Cys His Met
 165 170 175
 Ser Ser Asn Pro Tyr Met Ile Val Phe Gly Val Ala Glu Ile Leu Leu
 180 185 190
 Ser Gln Val Pro Asp Phe Asp Gln Ile Trp Trp Ile Ser Ile Val Ala
 195 200 205
 Ala Val Met Ser Phe Thr Tyr Ser Ala Ile Gly Leu Ala Leu Gly Ile
 210 215 220
 Val Gln Val Ala Ala Asn Gly Val Phe Lys Gly Ser Leu Thr Gly Ile
 5 230 235 240
 Ser Ile Gly Thr Val Thr Gln Thr Gln Lys Ile Trp Arg Thr Phe Gln
 245 250 255
 Ala Leu Gly Asp Ile Ala Phe Ala Tyr Ser Tyr Ser Val Val Leu Ile
 260 265 270
 Glu Ile Gln Asp Thr Val Arg Ser Pro Pro Ala Glu Ser Lys Thr Met
 275 280 285
 Lys Lys Ala Thr Lys Ile Ser Ile Ala Val Thr Thr Ile Phe Tyr Met
 290 295 300
 Leu Cys Gly Ser Met Gly Tyr Ala Ala Phe Gly Asp Ala Ala Pro Gly
 305 310 315 320
 Asn Leu Leu Thr Gly Phe Gly Phe Tyr Asn Pro Phe Trp Leu Leu Asp
 325 330 335
 Ile Ala Asn Ala Ala Ile Val Val His Leu Val Gly Ala Tyr Gln Val
 340 345 350

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